

24745-1613

SEQUENCE LISTING

<110> Edwin L. Madison
Edgar O. Ong

<120> NUCLEIC ACID MOLECULES ENCODING TRANSMEMBRANE SERINE PROTEASE 7, THE
ENCODED POLYPEPTIDES AND METHODS BASED THEREON

<130> 24745-1613

<140>

<141> Herewith

<150> 60/275,592

<151> 2001-03-13

<160> 22

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 3147

<212> DNA

<213> Homo Sapien

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<221> CDS

<222> (23)...(2589)

<223> Nucleotide sequence encoding MTSP1

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<301> O'Brien, T.J. and Tanimoto, H.

<308> GenBank #AR081724

<309> 2000-08-31

<310> 5,972,616

<311> 1998-02-20

<312> 1999-10-26

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Glu Lys Val Asn Gly Leu Glu Glu Gly Val Glu Phe Leu Pro Val Asn	
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Asn Val Lys Lys Val Glu Lys His Gly Pro Gly Arg Trp Val Val Leu	
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gca gcc gtg ctg atc ggc ctc ctc ttg gtc ttg ctg ggg atc ggc ttc	244
Ala Ala Val Leu Ile Gly Leu Leu Leu Val Leu Leu Gly Ile Gly Phe	
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Asn Ile Asp Cys Thr Trp Asn Ile Glu Val Pro Asn Asn Gln His Val	
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Glu Tyr Leu Ser Tyr Asp Ser Ser Asp Pro Cys Pro Gly Gln Phe Thr	
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Asp Glu Ala Ser Cys Pro Lys Val Asn Val Val Thr Cys Thr Lys His	
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Asp Cys Gly Leu Arg Ser Phe Thr Arg Gln Ala Arg Val Val Gly Gly	
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Gln Arg Ser Ala Pro Gly Val Gln Glu Arg Arg Leu Lys Arg Ile Ile	
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Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly Lys Ala Ile Trp	
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<220>

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Lys Arg Ile Ile Ser His Pro Phe Phe Asn Asp Phe Thr Phe Asp Tyr
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Val Arg Pro Ile Cys Leu Pro Asp Ala Ser His Val Phe Pro Ala Gly
115 120 125
Lys Ala Ile Trp Val Thr Gly Trp Gly His Thr Gln Tyr Gly Gly Thr
130 135 140
Gly Ala Leu Ile Leu Gln Lys Gly Glu Ile Arg Val Ile Asn Gln Thr
145 150 155 160
Thr Cys Glu Asn Leu Leu Pro Gln Gln Ile Thr Pro Arg Met Met Cys
165 170 175
Val Gly Phe Leu Ser Gly Gly Val Asp Ser Cys Gln Gly Asp Ser Gly
180 185 190
Gly Pro Leu Ser Ser Val Glu Ala Asp Gly Arg Ile Phe Gln Ala Gly
195 200 205
Val Val Ser Trp Gly Asp Gly Cys Ala Gln Arg Asn Lys Pro Gly Val
210 215 220
Tyr Thr Arg Leu Pro Leu Phe Arg Asp Trp Ile Lys Glu Asn Thr Gly
225 230 235 240
Val

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<210> 5
 <211> 24
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 <213> Artificial Sequence

<220>
 <223> Primer

<400> 5
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24

<210> 6

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<211> 32
<212> DNA
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<220>
<223> Primer

<400> 6
gtcccaaact tactatacct acaatgtacc ag 32

<210> 7
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<212> DNA
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<220>
<223> Primer

<400> 7
gtcccaaact tactatacct acaatgtacc ag 32

<210> 8
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<220>
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<400> 8
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<210> 9
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<220>
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tgccattacc agcatcctct tctactcaaa g 31

<210> 10
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<220>
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<400> 10
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<210> 11
<211> 10
<212> PRT
<213> Homo sapien

<400> 11
Met Pro Leu Pro Ala Ser Ser Ser Thr Gln

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1 5 10

<210> 12
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 12
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<210> 13
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<220>
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<400> 13
 atagcgccg cacactacat accagtcttt gaggcaatc 39

<210> 14
 <211> 11
 <212> PRT
 <213> Homo sapien

<400> 14
 Lys Arg Ile Val Gln Gly Arg Glu Thr Ala Met
 1 5 10

<210> 15
 <211> 2100
 <212> DNA
 <213> Homo sapien

<220>
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 <222> (45)...(1361)
 <223> MTSP7: full length cDNA

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 <221> CDS
 <222> (45)...(1361)
 <223> MTSP7: full length cDNA

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 Met Met Tyr Thr
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cct gtt gaa ttt tca gaa gct gaa ttc tca cga gct gaa tat caa aga 104
 Pro Val Glu Phe Ser Glu Ala Glu Phe Ser Arg Ala Glu Tyr Gln Arg
 5 10 15 20

aag cag caa ttt tgg gac tca gta cgg cta gct ctt ttc aca tta gca 152
 Lys Gln Gln Phe Trp Asp Ser Val Arg Leu Ala Leu Phe Thr Leu Ala
 25 30 35

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att gta gca atc ata gga att gca att ggt att gtt act cat ttt gtt Ile Val Ala Ile Ile Gly Ile Ala Ile Gly Ile Val Thr His Phe Val 40 45 50	200
gtt gag gat gat aag tct ttc tat tac ctt gcc tct ttt aaa gtc aca Val Glu Asp Asp Lys Ser Phe Tyr Tyr Leu Ala Ser Phe Lys Val Thr 55 60 65	248
aat atc aaa tat aaa gaa aat tat ggc ata aga tct tca aga gag ttt Asn Ile Lys Tyr Lys Glu Asn Tyr Gly Ile Arg Ser Ser Arg Glu Phe 70 75 80	296
ata gaa agg agt cat cag att gaa aga atg atg tct agg ata ttt cga Ile Glu Arg Ser His Gln Ile Glu Arg Met Met Ser Arg Ile Phe Arg 85 90 95 100	344
cat tct tct gta ggc ggt cga ttt atc aaa tct cat gtt atc aaa tta His Ser Ser Val Gly Gly Arg Phe Ile Lys Ser His Val Ile Lys Leu 105 110 115	392
agt cca gat gaa caa ggt gtg gat att ctt ata gtg ctc ata ttt cga Ser Pro Asp Glu Gln Gly Val Asp Ile Leu Ile Val Leu Ile Phe Arg 120 125 130	440
tac cca tct act gat agt gct gaa caa atc aag aaa aaa att gaa aag Tyr Pro Ser Thr Asp Ser Ala Glu Gln Ile Lys Lys Lys Ile Glu Lys 135 140 145	488
gct tta tat caa agt ttg aag acc aaa caa ttg tct ttg acc ata aac Ala Leu Tyr Gln Ser Leu Lys Thr Lys Gln Leu Ser Leu Thr Ile Asn 150 155 160	536
aaa cca tca ttt aga ctc aca cct att gac agc aaa aag atg agg aat Lys Pro Ser Phe Arg Leu Thr Pro Ile Asp Ser Lys Lys Met Arg Asn 165 170 175 180	584
ctt ctc aac agt cgc tgt gga ata agg atg aca tct tca aac atg cca Leu Leu Asn Ser Arg Cys Gly Ile Arg Met Thr Ser Ser Asn Met Pro 185 190 195	632
tta cca gca tcc tct tct act caa aga att gtc caa gga agg gaa aca Leu Pro Ala Ser Ser Ser Thr Gln Arg Ile Val Gln Gly Arg Glu Thr 200 205 210	680
gct atg gaa ggg gaa tgg cca tgg cag gcc agc ctc cag ctc ata ggg Ala Met Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln Leu Ile Gly 215 220 225	728
tca ggc cat cag tgt gga gcc agc ctc atc agt aac aca tgg ctg ctc Ser Gly His Gln Cys Gly Ala Ser Leu Ile Ser Asn Thr Trp Leu Leu 230 235 240	776
aca gca gct cac tgc ttt tgg aaa aat aaa gac cca act caa tgg att Thr Ala Ala His Cys Phe Trp Lys Asn Lys Asp Pro Thr Gln Trp Ile 245 250 255 260	824
gct act ttt ggt gca act ata aca cca ccc gca gtg aaa cga aat gtg Ala Thr Phe Gly Ala Thr Ile Thr Pro Pro Ala Val Lys Arg Asn Val 265 270 275	872
agg aaa att att ctt cat gag aat tac cat aga gaa aca aat gaa aat	920

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Arg	Lys	Ile	Ile	Leu	His	Glu	Asn	Tyr	His	Arg	Glu	Thr	Asn	Glu	Asn	
			280					285					290			
gac	att	gct	ttg	gtt	cag	ctc	tct	act	gga	gtt	gag	ttt	tca	aat	ata	968
Asp	Ile	Ala	Leu	Val	Gln	Leu	Ser	Thr	Gly	Val	Glu	Phe	Ser	Asn	Ile	
		295					300					305				
gtc	cag	aga	gtt	tgc	ctc	cca	gac	tca	tct	ata	aag	ttg	cca	cct	aaa	1016
Val	Gln	Arg	Val	Cys	Leu	Pro	Asp	Ser	Ser	Ile	Lys	Leu	Pro	Pro	Lys	
		310				315					320					
aca	agt	gtg	ttc	gtc	aca	gga	ttt	gga	tcc	att	gta	gat	gat	gga	cct	1064
Thr	Ser	Val	Phe	Val	Thr	Gly	Phe	Gly	Ser	Ile	Val	Asp	Asp	Gly	Pro	
325					330					335					340	
ata	caa	aat	aca	ctt	cgg	caa	gcc	aga	gtg	gaa	acc	ata	agc	act	gat	1112
Ile	Gln	Asn	Thr	Leu	Arg	Gln	Ala	Arg	Val	Glu	Thr	Ile	Ser	Thr	Asp	
				345					350					355		
gtg	tgt	aac	aga	aag	gat	gtg	tat	gat	ggc	ctg	ata	act	cca	gga	atg	1160
Val	Cys	Asn	Arg	Lys	Asp	Val	Tyr	Asp	Gly	Leu	Ile	Thr	Pro	Gly	Met	
			360					365					370			
tta	tgt	gct	gga	ttc	atg	gaa	gga	aaa	ata	gat	gca	tgt	aag	gga	gat	1208
Leu	Cys	Ala	Gly	Phe	Met	Glu	Gly	Lys	Ile	Asp	Ala	Cys	Lys	Gly	Asp	
		375					380					385				
tct	ggt	gga	cct	ctg	gtt	tat	gat	aat	cat	gac	atc	tgg	tac	att	gta	1256
Ser	Gly	Gly	Pro	Leu	Val	Tyr	Asp	Asn	His	Asp	Ile	Trp	Tyr	Ile	Val	
	390					395					400					
ggt	ata	gta	agt	tgg	gga	caa	tca	tgt	gca	ctt	ccc	aaa	aaa	cct	gga	1304
Gly	Ile	Val	Ser	Trp	Gly	Gln	Ser	Cys	Ala	Leu	Pro	Lys	Lys	Pro	Gly	
405					410				415					420		
gtc	tac	acc	aga	gta	act	aag	tat	cga	gat	tgg	att	gcc	tca	aag	act	1352
Val	Tyr	Thr	Arg	Val	Thr	Lys	Tyr	Arg	Asp	Trp	Ile	Ala	Ser	Lys	Thr	
				425				430						435		
ggt	atg	tag	tgtggtt	gtt	ccatgag	tta	tacacat	ggc	acacagag	ct						1401
Gly	Met	*														
gatactcctg	cgtat	ttttgt	attgt	tttaaa	ttcatt	tact	ttggatt	agt	gctttt	gcta						1461
gatgtcaaga	agccct	ttcag	acccag	acaa	atcta	atatac	ctgaggt	ggc	ctttac	atac						1521
gtaggaccaa	accctc	tcta	ccatgag	gga	agaag	acaca	gcaa	atgaca	gacagc	acct						1581
attccttact	cacaag	ggaa	actgct	tgtg	atactt	ccta	ataag	ataaa	taagt	gggtt						1641
ccctcaattg	aagacag	gaa	catcat	tttc	cacagg	atat	gaagag	ctgc	cagtaa	tgcc						1701
aaaatccttac	ctcatat	aat	acctg	gagca	tgtgag	attc	ttctag	tga	aaaga	acagt						1761
cttccctgaa	gactcag	ggc	ttcaac	attc	taga	actgat	aagt	ggacct	tcagt	gtgca						1821
agaatggaga	agcat	ggat	ttgcatt	atg	acttga	actg	ggctt	atatc	taata	atata						1881
gagcactatc	actaac	ctca	acagtt	gaca	ttttaaa	agt	ttttaa	aatgt	atctga	actt						1941
gctgttaaca	cagtgt	tata	actca	agcac	tagctt	cagg	aagcat	gttg	tggtg	ttaag						2001
aagctttttct	gatttatt	ct	ttaac	agcat	cttgcc	atct	atatgt	ttag	agcag	ttggc						2061
ccagaaaagga	caaaaaaa		aaaaaa	aaaaaa	aaaaaa	aaaaaa										2100

<210> 16
 <211> 438
 <212> PRT
 <213> Homo sapien

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<400> 16
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 Glu Tyr Gln Arg Lys Gln Gln Phe Trp Asp Ser Val Arg Leu Ala Leu
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 Phe Thr Leu Ala Ile Val Ala Ile Ile Gly Ile Ala Ile Gly Ile Val
 35 40 45
 Thr His Phe Val Val Glu Asp Lys Ser Phe Tyr Leu Ala Ser
 50 55 60
 Phe Lys Val Thr Asn Ile Lys Tyr Lys Glu Asn Tyr Gly Ile Arg Ser
 65 70 75 80
 Ser Arg Glu Phe Ile Glu Arg Ser His Gln Ile Glu Arg Met Met Ser
 85 90 95
 Arg Ile Phe Arg His Ser Ser Val Gly Gly Arg Phe Ile Lys Ser His
 100 105 110
 Val Ile Lys Leu Ser Pro Asp Glu Gln Gly Val Asp Ile Leu Ile Val
 115 120 125
 Leu Ile Phe Arg Tyr Pro Ser Thr Asp Ser Ala Glu Gln Ile Lys Lys
 130 135 140
 Lys Ile Glu Lys Ala Leu Tyr Gln Ser Leu Lys Thr Lys Gln Leu Ser
 145 150 155 160
 Leu Thr Ile Asn Lys Pro Ser Phe Arg Leu Thr Pro Ile Asp Ser Lys
 165 170 175
 Lys Met Arg Asn Leu Leu Asn Ser Arg Cys Gly Ile Arg Met Thr Ser
 180 185 190
 Ser Asn Met Pro Leu Pro Ala Ser Ser Ser Thr Gln Arg Ile Val Gln
 195 200 205
 Gly Arg Glu Thr Ala Met Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu
 210 215 220
 Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu Ile Ser Asn
 225 230 235 240
 Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn Lys Asp Pro
 245 250 255
 Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro Pro Ala Val
 260 265 270
 Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr His Arg Glu
 275 280 285
 Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr Gly Val Glu
 290 295 300
 Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser Ser Ile Lys
 305 310 315 320
 Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly Ser Ile Val
 325 330 335
 Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg Val Glu Thr
 340 345 350
 Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp Gly Leu Ile
 355 360 365
 Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys Ile Asp Ala
 370 375 380
 Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn His Asp Ile
 385 390 395 400
 Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys Ala Leu Pro
 405 410 415
 Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg Asp Trp Ile
 420 425 430
 Ala Ser Lys Thr Gly Met
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<210> 17
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 <212> DNA

<213> Homo sapien

<220>

<221> CDS

<222> (1)...(702)

<223> Nucleotide sequence encoding Protease Domain

<400> 17

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gcc agc ctc cag ctc ata ggg tca ggc cat cag tgt gga gcc agc ctc	96
Ala Ser Leu Gln Leu Ile Gly Ser Gly His Gln Cys Gly Ala Ser Leu	
20 25 30	
atc agt aac aca tgg ctg ctc aca gca gct cac tgc ttt tgg aaa aat	144
Ile Ser Asn Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn	
35 40 45	
aaa gac cca act caa tgg att gct act ttt ggt gca act ata aca cca	192
Lys Asp Pro Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro	
50 55 60	
ccc gca gtg aaa cga aat gtg agg aaa att att ctt cat gag aat tac	240
Pro Ala Val Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr	
65 70 75 80	
cat aga gaa aca aat gaa aat gac att gct ttg gtt cag ctc tct act	288
His Arg Glu Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr	
85 90 95	
gga gtt gag ttt tca aat ata gtc cag aga gtt tgc ctc cca gac tca	336
Gly Val Glu Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser	
100 105 110	
tct ata aag ttg cca cct aaa aca agt gtg ttc gtc aca gga ttt gga	384
Ser Ile Lys Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly	
115 120 125	
tcc att gta gat gat gga cct ata caa aat aca ctt cgg caa gcc aga	432
Ser Ile Val Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg	
130 135 140	
gtg gaa acc ata agc act gat gtg tgt aac aga aag gat gtg tat gat	480
Val Glu Thr Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp	
145 150 155 160	
ggc ctg ata act cca gga atg tta tgt gct gga ttc atg gaa gga aaa	528
Gly Leu Ile Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys	
165 170 175	
ata gat gca tgt aag gga gat tct ggt gga cct ctg gtt tat gat aat	576
Ile Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn	
180 185 190	
cat gac atc tgg tac att gta ggt ata gta agt tgg gga caa tca tgt	624
His Asp Ile Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys	
195 200 205	
gca ctt ccc aaa aaa cct gga gtc tac acc aga gta act aag tat cga	672

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Ala Leu Pro Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg
 210 215 220

gat tgg att gcc tca aag act ggt atg tag
 Asp Trp Ile Ala Ser Lys Thr Gly Met *
 225 230

702

<210> 18
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 <212> PRT
 <213> Homo sapien

<400> 18
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 20 25 30
 Ile Ser Asn Thr Trp Leu Leu Thr Ala Ala His Cys Phe Trp Lys Asn
 35 40 45
 Lys Asp Pro Thr Gln Trp Ile Ala Thr Phe Gly Ala Thr Ile Thr Pro
 50 55 60
 Pro Ala Val Lys Arg Asn Val Arg Lys Ile Ile Leu His Glu Asn Tyr
 65 70 75 80
 His Arg Glu Thr Asn Glu Asn Asp Ile Ala Leu Val Gln Leu Ser Thr
 85 90 95
 Gly Val Glu Phe Ser Asn Ile Val Gln Arg Val Cys Leu Pro Asp Ser
 100 105 110
 Ser Ile Lys Leu Pro Pro Lys Thr Ser Val Phe Val Thr Gly Phe Gly
 115 120 125
 Ser Ile Val Asp Asp Gly Pro Ile Gln Asn Thr Leu Arg Gln Ala Arg
 130 135 140
 Val Glu Thr Ile Ser Thr Asp Val Cys Asn Arg Lys Asp Val Tyr Asp
 145 150 155 160
 Gly Leu Ile Thr Pro Gly Met Leu Cys Ala Gly Phe Met Glu Gly Lys
 165 170 175
 Ile Asp Ala Cys Lys Gly Asp Ser Gly Gly Pro Leu Val Tyr Asp Asn
 180 185 190
 His Asp Ile Trp Tyr Ile Val Gly Ile Val Ser Trp Gly Gln Ser Cys
 195 200 205
 Ala Leu Pro Lys Lys Pro Gly Val Tyr Thr Arg Val Thr Lys Tyr Arg
 210 215 220
 Asp Trp Ile Ala Ser Lys Thr Gly Met
 225 230

<210> 19
 <211> 42
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Primer

<400> 19
 tctctcgaga aaagaattgt ccaaggaagg gaaacagcta tg

42

<210> 20
 <211> 33
 <212> DNA
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<220>
<223> Primer

<400> 20
agatgagtct gggaggctaa ctctctggac tat 33

<210> 21
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<212> DNA
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<220>
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<400> 21
attcgcgggcc gcctacatac cagtctttga ggcaat 35

<210> 22
<211> 33
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<220>
<223> Primer

<400> 22
atagtccaga gagttagcct cccagactca tct 33